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See p. 5

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/435,733A

DATE: 05/01/2001  
 TIME: 18:02:23

Input Set : A:\CIBT-P02-052 SeqList.txt  
 Output Set: N:\CRF3\05012001\I435733A.raw

3 <110> APPLICANT: Galdes, Alphonse  
 4 Mahanthappa, Nagesh  
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
 7 PERIPHERAL NEUROPATHIES  
 9 <130> FILE REFERENCE: CIBT-P02-052  
 11 <140> CURRENT APPLICATION NUMBER: 09/435,733A  
 12 <141> CURRENT FILING DATE: 1999-11-08  
 14 <160> NUMBER OF SEQ ID NOS: 28  
 16 <170> SOFTWARE: PatentIn Ver. 2.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1277  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: chicken Shh  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (1)..(1275)  
 27 <400> SEQUENCE: .1  
 28 atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc 48  
 29 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile  
 30 1 5 10 15  
 32 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96  
 33 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly  
 34 20 25 30  
 36 att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag 144  
 37 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
 38 35 40 45  
 40 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192  
 41 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg  
 42 50 55 60  
 44 tat gaa ggg aag atc aca aga aac tcc gag aga att ttt aaa gaa cta acc 240  
 45 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr  
 46 65 70 75 80  
 48 cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga 288  
 49 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly  
 50 85 90 95  
 52 gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336  
 53 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu  
 54 100 105 110  
 56 ggc atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384  
 57 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr  
 58 115 120 125  
 60 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac 432  
 61 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr  
 62 130 135 140  
 64 gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag 480  
 65 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys  
 66 145 150 155 160

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68 tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc	528
69 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
70 165 170 175	
72 tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac	576
73 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
74 180 185 190	
76 tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg	624
77 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
78 195 200 205	
80 cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg	672
81 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
82 210 215 220	
84 gac cgc gtg ctg gct gct gac gac gac ggc cgg ctg ctc tac agt gac	720
85 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
86 225 230 235 240	
88 ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac	768
89 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
90 245 250 255	
92 gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc	816
93 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
94 260 265 270	
96 cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg	864
97 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
98 275 280 285	
100 tcc acc agt ggc cag ggc ctc ttc gcc agc aac gtg aag cct ggc caa	912
101 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
102 290 295 300	
104 cgt gtc tat gtg ctg ggc gag ggc cgg cag cag ctg ctg ccg gcg tct	960
105 Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser	
106 305 310 315 320	
108 gtc cac agc gtc tca ttg cgg gag gag ggc tcc gga gcc tac gcc cca	1008
109 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
110 325 330 335	
112 ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc	1056
113 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
114 340 345 350	
116 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca	1104
117 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
118 355 360 365	
120 ttc cgc ttg gct cag ggg ctg gcc gcc ctc tgc cca gat ggg gcc	1152
121 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
122 370 375 380	
124 atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg	1200
125 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
126 385 390 395 400	
128 ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat	1248
129 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	
130 405 410 415	
132 ccg ctg ggc atg gtg gca ccg gcc agc'tg	1277

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Output Set: N:\CRF3\05012001\I435733A.raw

133 Pro Leu Gly Met Val Ala Pro Ala Ser  
134 420 425  
136 <210> SEQ ID NO: 2  
137 <211> LENGTH: 1190  
138 <212> TYPE: DNA  
139 <213> ORGANISM: mouse Dhh  
141 <220> FEATURE:  
142 <221> NAME/KEY: CDS  
143 <222> LOCATION: (1)..(1188)  
145 <400> SEQUENCE: 2  
146 atg gct ctg ccg agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg 48  
147 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu  
148 1 5 10 15  
150 gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg 96  
151 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
152 20 25 30  
154 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt 144  
155 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
156 35 40 45  
158 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192  
159 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
160 50 55 60  
162 ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac 240  
163 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn  
164 65 70 75 80  
166 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac 288  
167 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp  
168 85 90 95  
170 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc 336  
171 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile  
172 100 105 110  
174 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384  
175 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
176 115 120 125  
178 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc 432  
179 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly  
180 130 135 140  
182 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480  
183 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly  
184 145 150 155 160  
186 ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac 528  
187 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr  
188 165 170 175  
190 gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg 576  
191 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu  
192 180 185 190  
194 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg 624  
195 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu  
196 195 200 205

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198	cg	ag	gc	g	gaa	cg	gaa	gg	ct	g	aa	ct	ca	tg	gg	g	ac	tgg	672
199	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp			
200	210					215					220								
202	gta	ctg	g	cc	g	at	g	ca	g	cg	g	ca	gt	cc	ac	g	tg	ctg	720
203	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu			
204	225					230				235				240					
206	ctc	ttc	ctg	g	ac	cg	g	at	ct	cg	cg	g	cc	tc	tc	gt	gt	gtg	768
207	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val			
208						245				250				255					
210	gag	acc	gag	cg	cct	ccg	cg	aaa	ct	tg	ctc	ac	cc	tg	cat	ct	tg	816	
211	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu			
212						260				265				270					
214	gt	ttc	gt	cg	gg	cc	g	cg	cct	gt	cc	gg	ttt	g	ca	cc	tg	864	
215	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro			
216						275				280				285					
218	gt	ttc	gc	cg	cg	c	t	at	gt	g	ac	tc	tg	gt	cc	gg	tg	912	
219	Val	Phe	Ala	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly		
220						290				295				300					
222	gg	gac	gc	ct	ca	cg	cg	cg	gt	g	cc	cg	tg	gg	cg	gg	aa	960	
223	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu				
224	305					310				315				320					
226	gg	cc	gt	gg	gt	ttc	g	ca	cc	tc	act	g	cg	ac	tg	tg	tc	1008	
227	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val			
228						325				330				335					
230	aa	ac	g	tc	gc	cc	tc	tc	tg	cg	gt	ct	aa	gg	at	cc	tg	1056	
231	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp			
232						340				345				350					
234	gg	cc	ca	cg	cc	ttc	g	cc	ct	tg	cc	ac	tg	cc	gg	gg	gt	1104	
235	Ala	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala		
236						355				360				365					
238	ct	ct	c	c	gg	gg	gt	g	ca	cc	at	gg	at	tg	tg	tg	tc	1152	
239	Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser			
240						370				375				380					
242	cg	cg	ct	tt	tg	cc	gg	gg	tg	tt	at	tg	gg	tg				1190	
243	Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly							
244						385				390				395					
246	<210>	SEQ	ID	NO:	3														
247	<211>	LENGTH:	1281																
248	<212>	TYPE:	DNA																
249	<213>	ORGANISM:	mouse Ihh																
251	<220>	FEATURE:																	
252	<221>	NAME/KEY:	CDS																
253	<222>	LOCATION:	(1)..(1233)																
255	<400>	SEQUENCE:	3																
256	at	tg	cc	gg	cc	tt	cg	cc	ca	ct	gg	tt	tgt	ct	tg	tt	ct	48	
257	Met	Ser	Pro	Ala	Trp	Leu	Arg	Pro	Arg	Leu	Arg	Phe	Cys	Leu	Phe	Leu			
258	1				5					10			15						
260	ct	ct	ct	ct	gt	cc	cg	cg	gg	gg	tg	gg	cc	gg	gg	cg	gg	96	
261	Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg			

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262	20	25	30														
264	gtg	gtg	ggc	agc	cgc	cgg	agg	ccg	cct	cgc	aag	ctc	gtg	cct	ctt	gcc	144
265	Val	Val	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	
266	35				40					45							
268	tac	aag	cag	ttc	agc	ccc	aac	gtg	ccg	gag	aag	acc	ctg	ggc	gcc	agc	192
269	Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	
270	50				55					60							
272	ggg	cgc	tac	gaa	ggc	aag	atc	gct	cgc	agc	tct	gag	ccg	ttc	aaa	gag	240
273	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	
274	65				70					75						80	
276	ctc	acc	ccc	aac	tac	aat	ccc	gac	atc	atc	ttc	aag	gac	gag	gag	aac	288
277	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	
278																	
280	acg	ggt	gcc	gac	cgc	ctc	atg	acc	cag	cgc	tgc	aag	gac	cgt	ctg	aac	336
281	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	
282																	
284	tca	ctg	gcc	atc	tct	gtc	atg	aac	cag	tgg	cct	ggg	gtt	aaa	ctg	cg	384
285	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
286																	
288	gtg	acc	gaa	ggc	cgg	gat	gaa	gat	ggc	cat	cac	tca	gag	gag	tct	tta	432
289	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
290																	
292	cac	tat	gag	ggc	cgc	gct	gtg	gat	atc	acc	acc	tca	gac	cgt	gac	cga	480
293	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
294																	
296	aat	aag	tat	gga	ctg	ctg	gct	ccg	tta	gca	gtg	gag	gcc	ggc	tcc	gac	528
297	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
298																	
300	tgg	gtg	tat	tac	gag	tcc	aag	gcc	cac	gtg	cat	tgc	tct	gtc	aag	tct	576
301	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
302																	
304	gag	cat	tcg	gcc	gct	gcc	aag	aca	ggt	ggc	tgc	ttt	cct	gcc	gga	gcc	624
305	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
306																	
308	cag	gtg	cgc	cta	gag	aac	ggg	gag	cgt	gtg	gcc	ctg	tca	gct	gta	aag	672
309	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
310																	
312	cca	gga	gac	cg	gtg	cc	atg	ggg	gag	gat	ggg	acc	ccc	acc	ttc	720	
313	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
314																	
316	agt	gat	gtg	ctt	att	tcc	ctg	gac	cgc	gag	cca	aac	ccg	ctg	aga	gct	768
317	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
318																	
320	tcc	cag	gtc	atc	gag	act	cag	gat	cct	ccg	cgt	ccg	ctg	gct	ctc	acg	816
321	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
322																	
324	cct	gcc	cac	ctg	ctc	tcc	att	gct	gac	aat	cat	aca	gaa	cca	gca	gcc	864
325	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
326																	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 05/01/2001  
PATENT APPLICATION: US/09/435,733A TIME: 18:02:24

Input Set : A:\CIBT-P02-052 SeqList.txt  
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L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:1613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:2192 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22